



Journal of Management Inquiry 26(4) 391-407 © The Author(s) 2017. Reprints and permissions: [DOI: 10.1177/1056492617718101](http://sagepub.com/journalsPermissions.nav) <http://jmi.sagepub.com>



APPLICATION NUMBER: US 08/216,305  
 FILING DATE: 30-SEP-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/428,734  
 FILING DATE: 25-APR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWN, SCOTT A.  
 REGISTRATION NUMBER: 32,724  
 REFERENCE/ATTY NUMBER: 21,5019  
 TELEPHONE: (617) 498-2324  
 TELEFAX: (617) 876-5451  
 INFORMATION FOR SEQ ID NOS: 1-6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 313 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-713-556F-36

Query Match 42.5% Score 1236; DB 4; Length 313;  
 Best Local Similarity Rf 28; Pct 100;  
 Matches 233; Conservative 3; Mismatches 17; Indels 10; Gaps 1;

QY 432 YGVYPERDEGEGVAFATKV-----VKPFKARPHICPCPAPALGAPSVLEF 341  
 DB 51 YDLPEPEPEMLRNSTDTPLTGCPSTVEPARAKHCTCPAPALGAPSVLEF 110  
 QY 342 PKPKDTIMISTREVCVYVDSHEG EYKFNKYVGVVHNAAKTPPEQGNSTYKVS 401  
 DB 111 PKPKDTIMISTREVCVYVDSHEG EYKFNKYVGVVHNAAKTPPEQGNSTYKVS 170  
 QY 402 VTLVHCWNGEYVGVVGNFALPFIETISKAKTGPPEPVYTPPPEPEMTYNOVS 461  
 DB 171 VTLVHCWNGEYVGVVGNFALPFIETISKAKTGPPEPVYTPPPEPEMTYNOVS 230  
 QY 462 LTLVAFVPSDIAVENESNPFENNYKTFVLESEGEFFLYSTLVKSPMGQGNVS 521  
 DB 231 LTLVAFVPSDIAVENESNPFENNYKTFVLESEGEFFLYSTLVKSPMGQGNVS 290  
 QY 522 GSVNHEALHNHYTKSLSPK 544  
 DB 291 GSVNHEALHNHYTKSLSPK 313

RESULT 7  
 US-09-131-247-16  
 Sequence 16, Application US/09/131247  
 Patent No. 6294170  
 GENERAL INFORMATION:  
 APPLICANT: Boone, Thomas C.  
 APPLICANT: Heirshenson, Susan  
 APPLICANT: Collins, David S.  
 TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY  
 TITLE OF INVENTION: DISEASES  
 FILE REFERENCE: A-365F  
 CURRENT APPLICATION NUMBER: US/09/131,247  
 CURRENT FILING DATE: 1998-08-07  
 EARLIER APPLICATION NUMBER: 60/055,185  
 EARLIER FILING DATE: 1997-08-08  
 EARLIER APPLICATION NUMBER: FCT US 09/091,111  
 EARLIER FILING DATE: 1997-02-10  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: Patent In Ver. 4.0  
 SEQ ID NO 16  
 LENGTH: 389  
 TYPE: FET  
 ORGANISM: Human  
 US-09-131-247-16  
 Query Match 42.4% Score 1232.5; DB 4; Length 388;

Best Local Similarity 63.1% Pct 100;  
 Matches 250; Conservative 21; Mismatches 70; Indels 59; Gaps 6;  
 QY 173 LANNTELPAFLNG-----LNNLTLGNSNLTIPGPGNSHLLPAPLHNPMDL 275  
 DB 26 LNN LVAAYLQGVNLLERLVVAPLPPHML-----FLGTHAKKML 68  
 QY 276 LLLVTHVHGVGGEETVTVVGVVANTGVNAGVGVVGVVGVVGVVGVVGVVGVV 281  
 DB 63 GVNAGGGLNGLVAVIA LGGVGGVGVVGVVGVVGVVGVVGVVGVVGVVGVV 122  
 QY 282 -----LGGGGLNGLVAVIA LGGVGGVGVVGVVGVVGVVGVVGVVGVVGVV 128  
 DB 283 LGLMAGGVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 172  
 QY 329 PLALGASVFLPPEKPNVLSNLTETVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 388  
 DB 173 FDLGQGVFLPPEKPNVLSNLTETVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 232  
 QY 389 LLLVTHVHGVGGEETVTVVGVVANTGVNAGVGVVGVVGVVGVVGVVGVVGVV 448  
 DB 233 REBOVNSTVTVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 292  
 QY 449 LLLVTHVHGVGGEETVTVVGVVANTGVNAGVGVVGVVGVVGVVGVVGVVGVV 508  
 DB 293 LLLVTHVHGVGGEETVTVVGVVANTGVNAGVGVVGVVGVVGVVGVVGVVGVV 462  
 QY 509 VDRVNGVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 544  
 DB 353 VDRVNGVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVVGVV 398

RESULT 8  
 US-08-466-151-8  
 Sequence 4, Application US/08/466151  
 Patent No. 6037453  
 GENERAL INFORMATION:  
 APPLICANT: Jardieu, Paula M.  
 APPLICANT: Presta, Leonard G.  
 TITLE OF INVENTION: Immunoglobulin Variants  
 NUMBER OF SEQUENCES: 05  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,151  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/466,163  
 FILING DATE: 06-Jun-1995  
 APPLICATION NUMBER: 08/405,617  
 FILING DATE: 15-MAR-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/95/08,877  
 FILING DATE: 26-JAN-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 07/974,495  
 FILING DATE: 07-MAY-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 07/744,764  
 FILING DATE: 14-AUG-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Svoboda, Craig G.





Sequence version 5.1.1  
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DB protein protein search, using SW model

Run on: December 23, 2002, 12:10:58 ; Search time 13.8419 seconds

(without alignments)  
4780.806 Million cell updates/sec

Hit list: 10-068-426-1

Sequence: 1 MRLDLDLPSLHHPDLC...MHAAHNYTSLSLSLK 541

Scoring table: BLAST/BLAST2  
Gapop 10.0 ; Gapext 0.5

Scatched: 283224 swaps, 6144422 residues

Minimum DB seq length: 0

Maximum DB seq length: 26000000

Post processing: Minimum Match 0.4

Maximum Match 1000  
Listing first 40 summaries

Database: 1: P1111\*

2: P1121\*

3: P1131\*

4: P1141\*

Prod. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1693	98.3	926	1	MBHUA
2	1265	41.5	474	2	SP9339
3	1197.5	41.2	300	1	GHHU
4	1197	41.2	255	4	S41806
5	1150	39.6	234	2	P10207
6	1149.5	39.6	426	1	12H0
7	1141.5	39.3	477	2	A23611
8	1139.5	39.2	477	2	A60764
9	1137	39.1	427	1	G4H01
10	1115	38.4	289	1	G4H01
11	918	31.6	328	2	147160
12	918	31.6	328	2	147160
13	913	31.3	423	1	G4H01
14	911	31.3	277	2	147162
15	888.5	30.6	328	2	147168
16	887	30.5	329	1	G4H01
17	886	30.5	328	2	147161
18	851	29.3	470	2	S22000
19	844	29.0	429	1	G4H01
20	835	28.7	308	2	G4H01
21	835	28.7	472	2	S41439
22	834	28.7	444	2	S41436
23	833	28.6	398	1	G4H01
24	831	28.6	326	2	PS0017
25	828	28.5	331	2	PS0018
26	823	28.4	329	2	S30047
27	820.5	28.4	424	1	G1HMS
28	815.5	28.1	393	1	G1HMS
29	812	27.9	422	2	PS0019

40	805	27.7	350	1	G2MSA
41	805	27.7	459	2	S3748
42	802	27.6	357	1	G2MSA
43	800	27.5	309	1	G2MSA
44	790	27.2	446	1	G2MSA
45	769.5	26.5	474	1	G2MSA
46	762.5	26.2	427	2	S06611
47	762.5	26.2	405	1	G2MSA
48	746	25.7	475	2	S01321
49	704	24.2	180	2	146732
40	580.5	20.0	249	2	S03340
41	573	19.7	152	2	S14236
42	568.5	19.6	218	2	A60400
43	409	14.1	572	2	H46429
44	399.5	12.4	388	1	G1HMS
45	358	12.3	453	2	S37306

#### ALIGNMENTS

#### RESULT 1

MBHUA

platelet glycoprotein Ib alpha chain precursor - human

NCBI:us-10-068-426-1

C:Species: Homo sapiens (man)

C:Date: 26 Dec 1987 #sequence revision 26 Dec 1987 #1001 update

C:Accession: A94174; A60455; A94174; S16945; A27075; A27192

RefSeq: A94174; A60455; A94174; S16945; A27075; A27192

Prod. No. 1693

Score 1693

Query Match 98.3

Length 926

DB ID 1

Description MBHUA

platelet glycoprotein Ib alpha chain precursor - human

NCBI:us-10-068-426-1

C:Species: Homo sapiens (man)

C:Date: 26 Dec 1987 #sequence revision 26 Dec 1987 #1001 update

C:Accession: A94174; A60455; A94174; S16945; A27075; A27192

RefSeq: A94174; A60455; A94174; S16945; A27075; A27192

Prod. No. 1693

Score 1693

Query Match 98.3

Length 926

DB ID 1

Description MBHUA

platelet glycoprotein Ib alpha chain precursor - human

NCBI:us-10-068-426-1

C:Species: Homo sapiens (man)

C:Date: 26 Dec 1987 #sequence revision 26 Dec 1987 #1001 update

C:Accession: A94174; A60455; A94174; S16945; A27075; A27192

RefSeq: A94174; A60455; A94174; S16945; A27075; A27192

Prod. No. 1693

Score 1693

Query Match 98.3

Length 926

DB ID 1

Description MBHUA

platelet glycoprotein Ib alpha chain precursor - human

NCBI:us-10-068-426-1

C:Species: Homo sapiens (man)

C:Date: 26 Dec 1987 #sequence revision 26 Dec 1987 #1001 update

1



1. The following information is being provided to you for your information only. It is not intended to be used for any other purpose.

(Withhold all information)  
 2. The following information is being provided to you for your information only. It is not intended to be used for any other purpose.

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used for the preparation of antibodies for use in therapy, detection, diagnosis and drug development. AAG0849 to AAG4886 encode specifically selected fusion proteins from the present invention, which are given in AAG2794 to AAG2797.

XX AAG2794-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2794 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX AAG2795-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2795 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX AAG2796-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2796 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX AAG2797-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2797 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX AAG2798-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2798 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX AAG2799-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2799 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX AAG2800-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2800 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX AAG2801-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2801 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX AAG2802-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2802 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX AAG2803-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2803 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX AAG2804-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2804 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX AAG2805-41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2805 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

administering a composition comprising an effective amount of a p-selectin antagonist. The polypeptides and polypeptide forms of the invention have thrombolytic and anticoagulant activity. The method is useful for treating or inhibiting thrombosis in a subject, particularly a human. The method is also useful for inhibiting cell adhesion to blood vessels in a subject, increasing the movement of cells relative to blood vessels in a subject, or inhibiting the arrest of a thrombus in a subject or in a subject. The subject is at risk for thrombosis, such as a subject suffering from a cardiovascular disease or disorder (e.g., atherosclerosis or hypertension), or a subject who has undergone cardiovascular or general vascular procedures or intervention such as angioplasty of any vessel.

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2806 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2807 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2808 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2809 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2810 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2811 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2812 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2813 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2814 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2815 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2816 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1

XX Seq: 1266 41\* AA

Seq: 1266 42.7% Score: 12.66, Id: 2% Length: 41  
Pos: 2817 Similarity: 86.6% Evid: No. 1,40786  
Hit: 2997 Coverage: 97 Mismatches: 171 Indels: 10 Gaps: 1



















































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Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in the medium containing 100 mg/l of tetracycline. The cell concentration of the *Agrobacterium* strains was adjusted to 10<sup>8</sup> cells/ml. The cell suspension was mixed with the plant tissue and the transformation efficiency was determined. The results are shown as the mean ± SD of three independent experiments. The asterisk indicates a significant difference (*p* < 0.05) between the two groups.

1. The first group of students (Group A) was assigned to read the text and identify the main idea of the passage. They were then asked to write a short paragraph summarizing the main idea in their own words.

1. The first step is to identify the problem. This involves understanding the current situation and what needs to be changed.

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Category	Sub-category	Value
A. General	1.1.1.1	10
	1.1.1.2	10
	1.1.1.3	10
	1.1.1.4	10
	1.1.1.5	10
	1.1.1.6	10
	1.1.1.7	10
	1.1.1.8	10
	1.1.1.9	10
	1.1.1.10	10
B. Specific	2.1.1.1	10
	2.1.1.2	10
	2.1.1.3	10
	2.1.1.4	10
	2.1.1.5	10
	2.1.1.6	10
	2.1.1.7	10
	2.1.1.8	10
	2.1.1.9	10
	2.1.1.10	10

[illegible]

1. *Chlorophyll *a** and *Chlorophyll *b** were determined in the whole homogenate and in the supernatant and pellet fractions after centrifugation at 1000g for 10 min. The supernatant and pellet fractions were separated by centrifugation at 1000g for 10 min. The supernatant and pellet fractions were separated by centrifugation at 1000g for 10 min. The supernatant and pellet fractions were separated by centrifugation at 1000g for 10 min.

[illegible]

# ANNALS

Age Group	1980	1990	2000	2010	2020
0-14	25	22	18	15	10
15-24	20	18	15	12	8
25-34	15	14	13	12	10
35-44	12	11	10	10	10
45-54	10	10	10	10	10
55-64	8	8	8	8	8
65-74	15	18	22	28	35
75+	5	5	5	5	5

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